

A C A A A A C A A A T C A C A G C A T A T G C C

0 32/31 0 0 0 0 32/30 0 0 0 0 0 0 32/16 0 0 0 0 0 0 0 0

Fig. 2D1

	1	2	3	4	5	6	7	8	9	10	11	12
R21												
R21A												
R21B												
R21C												
R21D												
R21E												

Fig. 2D2

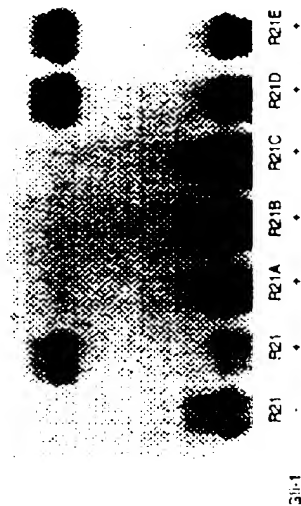


Fig. 2D3

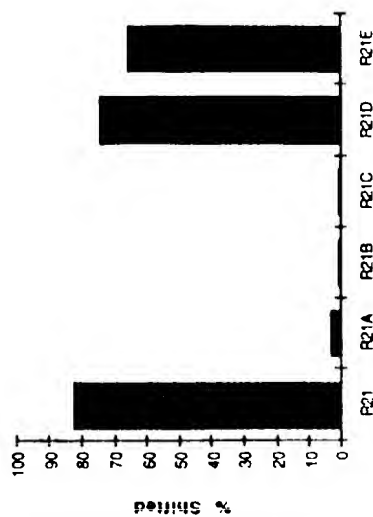


Fig. 2E

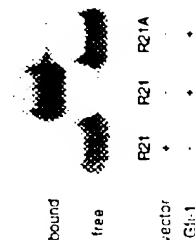


Fig. 2B

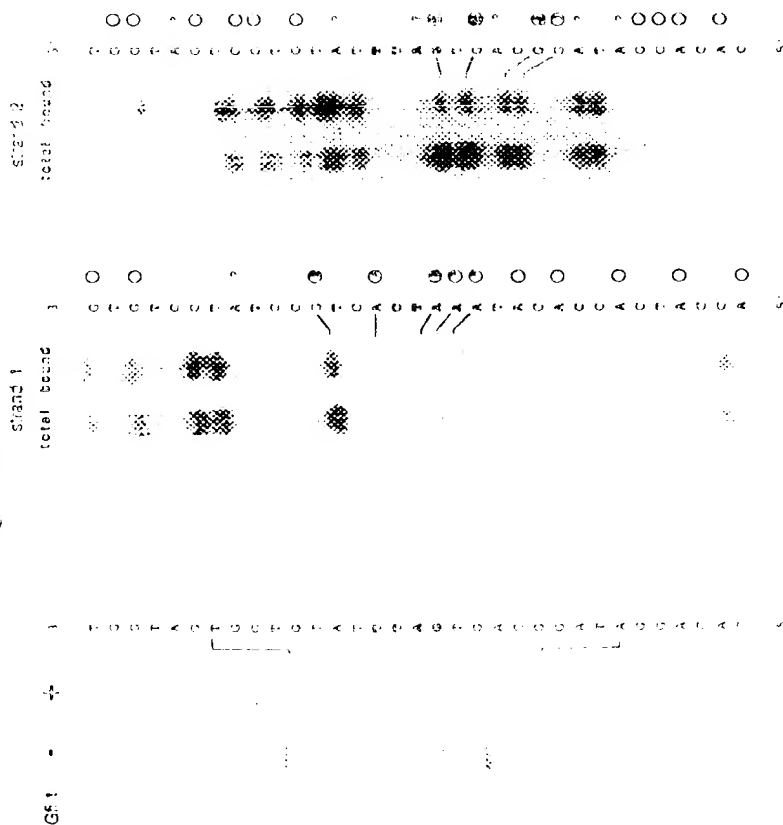


Fig. 2C

1 2 3 4 5 6 7 8 9 10 11 12

...ACCATCACCACATATATCAGTGCCTATCCTGIG...

...TGGTAGTGGTGTATTAGTGACGGATAGGACAC...

Fig. 3A HCMV MIE Promoter

GCGCGCGCTGGCTGACCGCCCCAACGACGCCCCCGCCCATTTGACGTCATAAATG
 ACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCATG
 GGTGGAGTATTACGTTAACTGCCCACTTGGCAGTACATCAAGTGATC
 ATATGCCAAAGTACGCCGCCCTATTGACGTCATGACGGTAAATGGCCCGCC
 TGGCATTATGCCCACTACATGACCTTATGGGACTTTCCCTACTTGGCAGTA
 CATCTACGTAATTACGTCATGCTATTACCATGGTGATGCGTTTGGCAGT
 ACATCAATGGCGTGGATAGCGGTTTGACTCAGCGGGATTTCAGTCTC
 CACCGCAITGACGTCATGCGGAGTTGTTTGGCACCAGAAATCAACGGGA
 CTTTCCAAATGTCGTAAACAACCTCGGCCCATTTGACGCAAAATGGCGGTA
 GCGGTGTACGGTGGGAGGCTCTATATAAGCAGAGCTGTTTAGTGAACCGT

Fig.3B

Gli-1 consensus TAAATCAC¹GGCA
 Gli-1 site #1 (-157 to -168) GAAATCCCCGTG
 Gli-1 site #2 (-111 to -100) AAAATCAACGGG

Fig. 3C

Point Mutations
 Gli-1 site #1 Gli-1 site #2
 Wildtype CMV CACGGGGATTTC.....AAATCAACGGG
 Mutant A CACGGGAGTTC.....AAATCAACGGG
 Mutant B CACGGGACTTC.....AAATCAACGGG

Fig. 3D

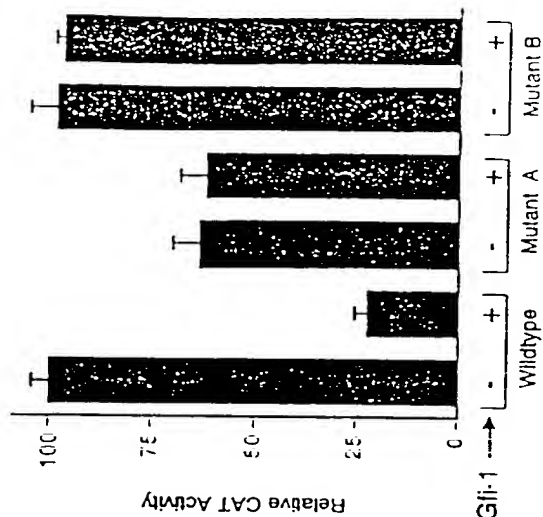


Fig. 4A

	GII-1 aa	Binding Site		3'	5'
		Predicted	R21		
Finger 1	T G V	- X	-	-	-
Finger 2	H S Q	T/C	-	-	-
Finger 3	R T T	G	-	-	-
Finger 4	Q D K	A	-	-	-
Finger 5	Q N T	G/t	-	-	-
Finger 6	R D R	A	-	-	-

Fig. 4B

